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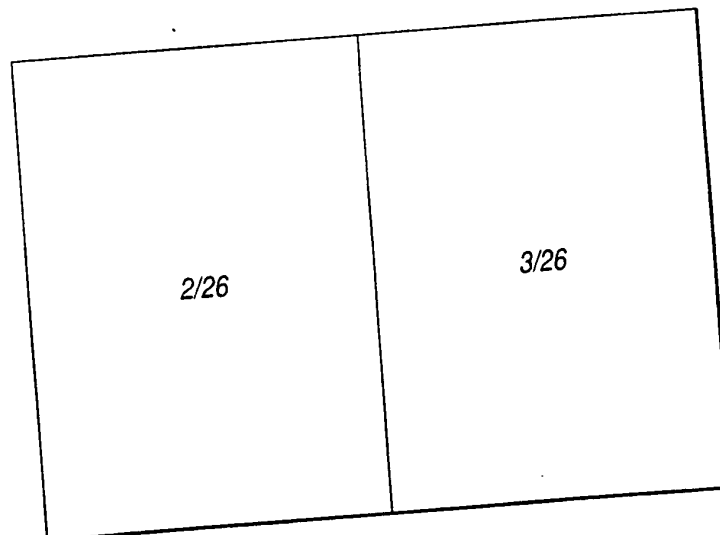


Fig. 1

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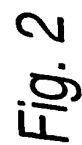
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Bclw-Rox	MATPASTPDT	RALVADFVGY
Bclw	DEFETRFRRT	FSDLAAQLHV
Bclw-Rox	DEFETRFRRT	FSDLAAQLHV
Bclw	VFGAALCAES	VNKEMEPLVG
Bclw-Rox	VFGAALCAES	VNKEMEPLVG
Bclw	YGDGALEEAR	RLREGNWASV
Bclw-Rox	ARVREMEEEA	EKLKELQNEV
Bclw-Rox	IYVGNDYGA	TAELEAHFH
Bclw-Rox	ESVRTSLALD	ESLFRGRQIK
Bclw-Rox	NSSRSRFYSG	FNSRPRGRIY

Fig. 1 (i)

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[illegible]

Fig. 1 (ii)



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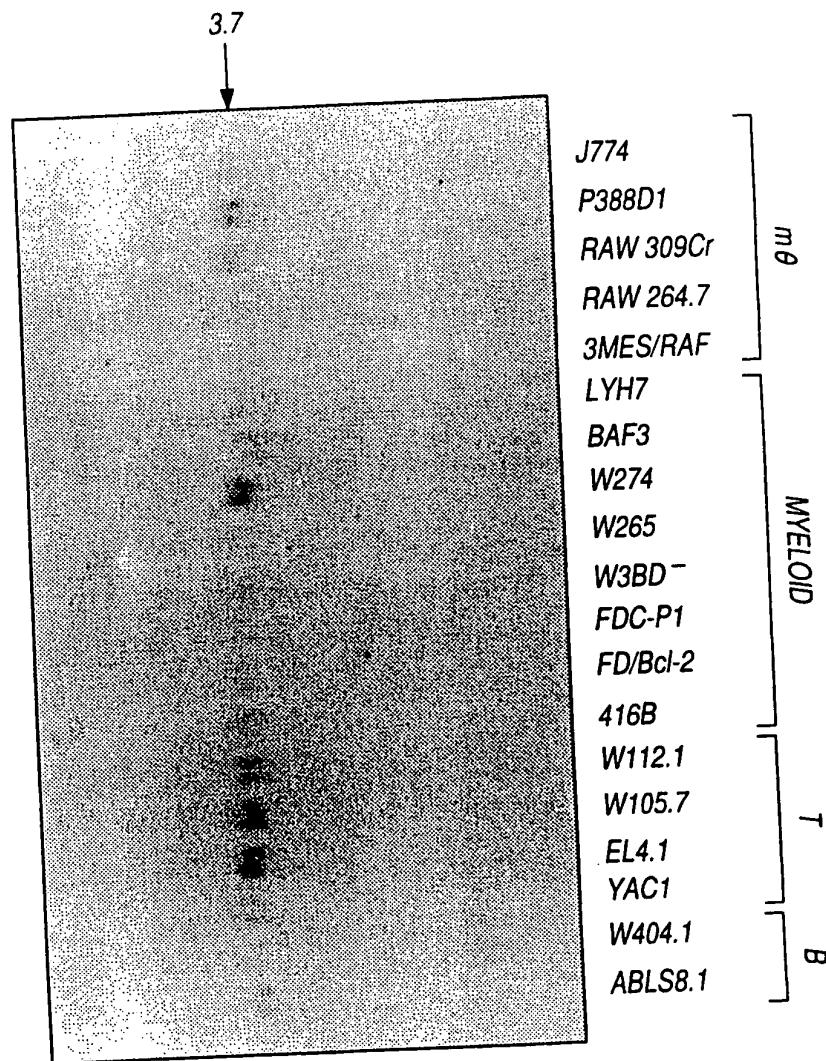


Fig. 3

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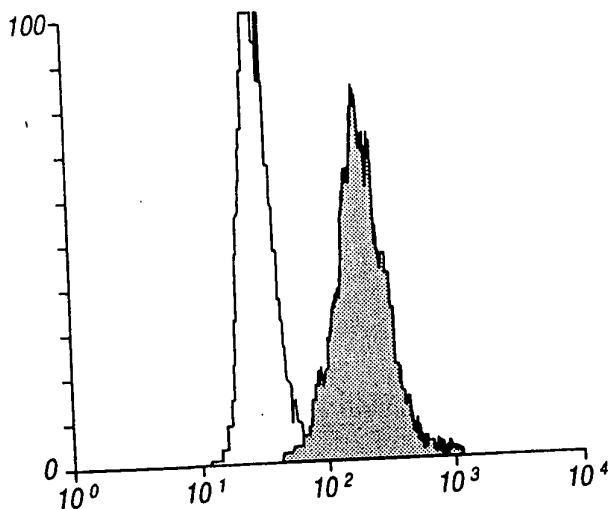


Fig. 4A

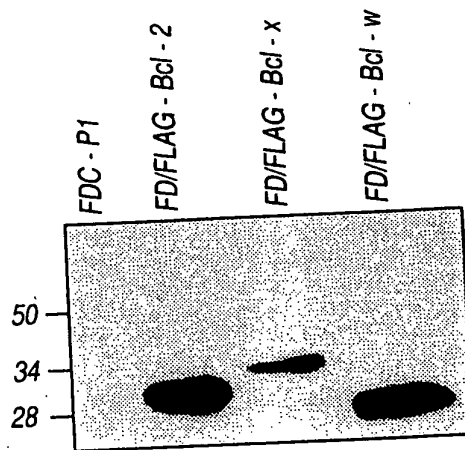


Fig. 4B

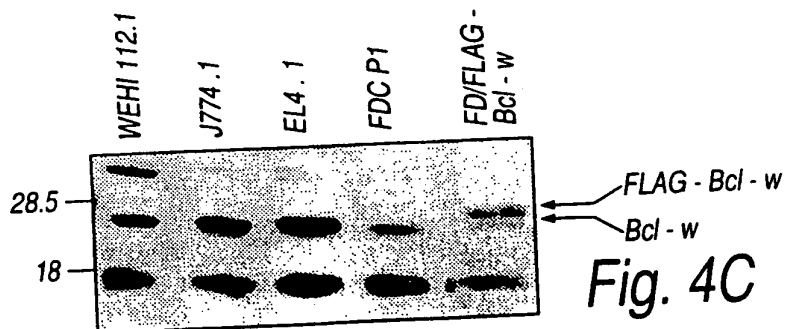


Fig. 4C

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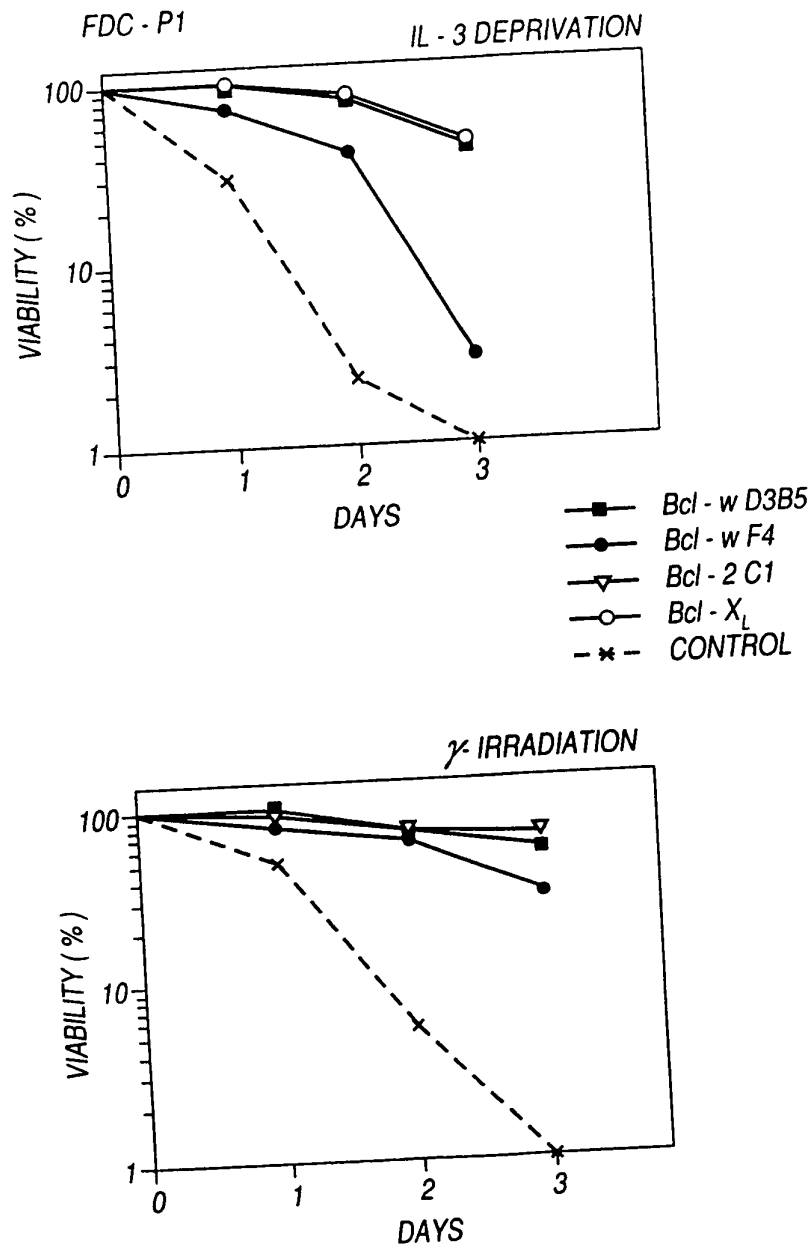


Fig. 5A

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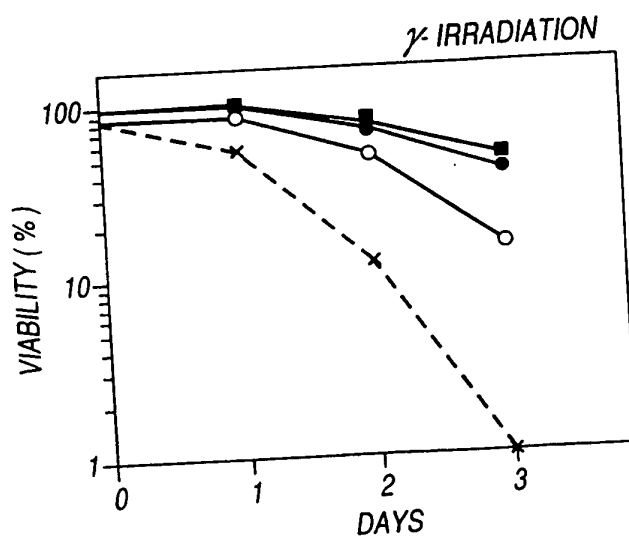
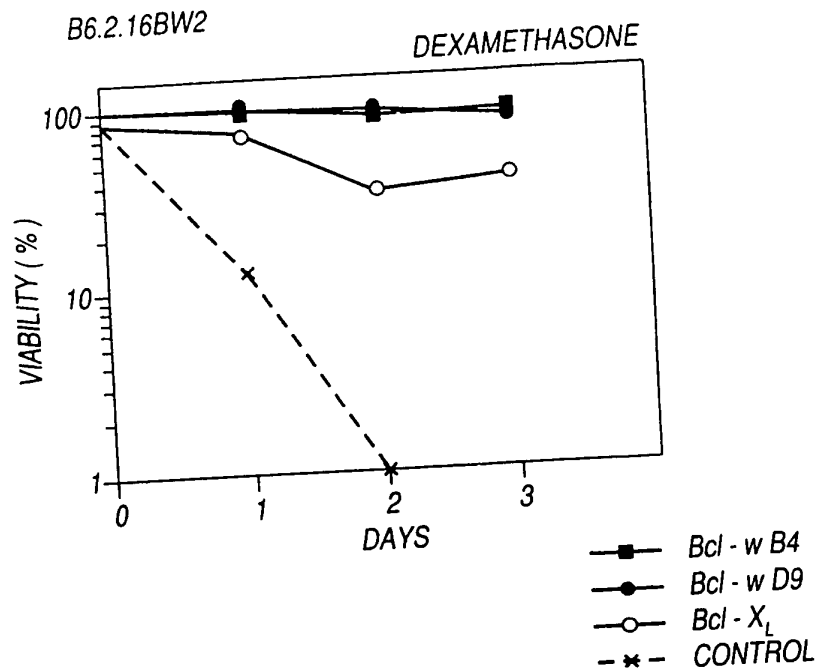


Fig. 5B

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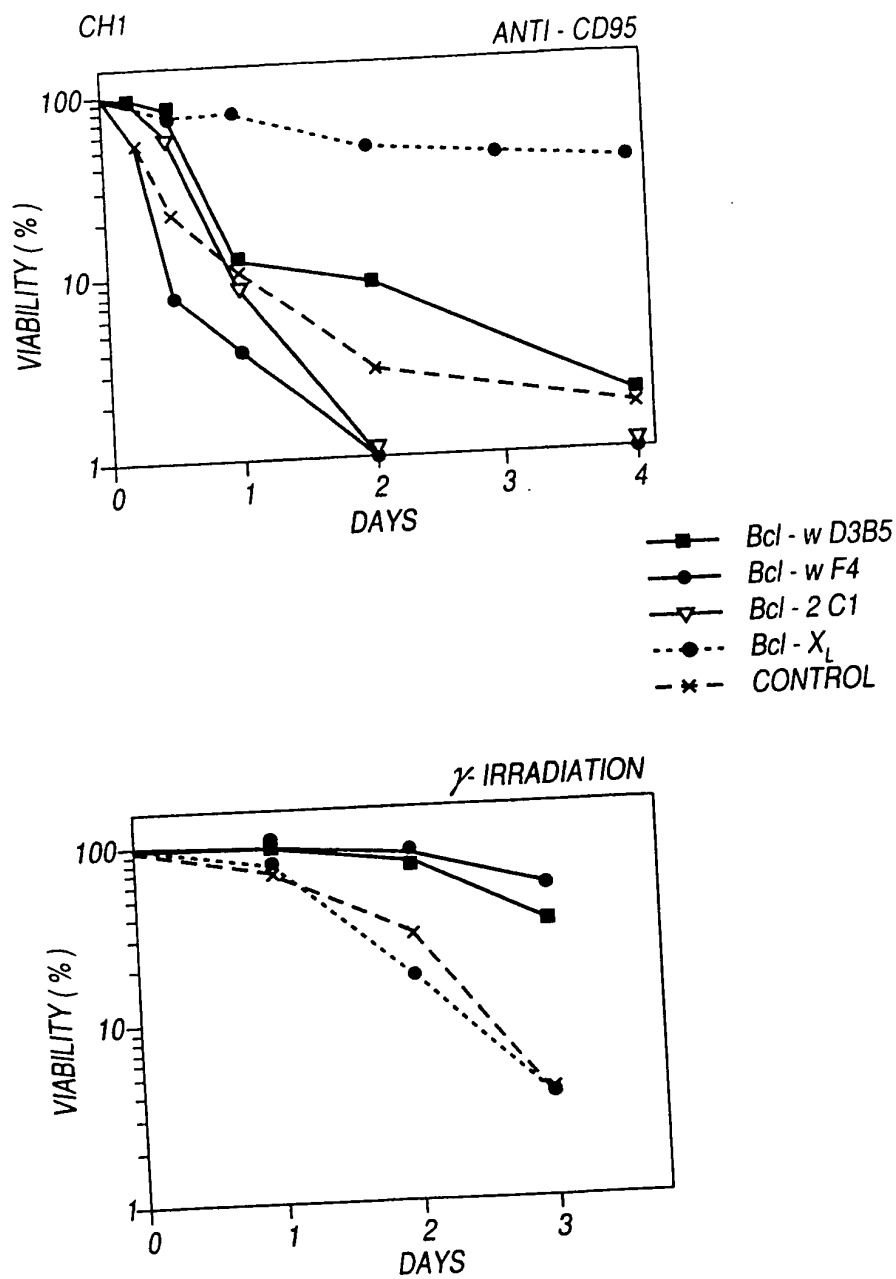


































Fig. 5C

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<i>Sftp1</i>								
<i>Tcra</i>								
<i>Bclw</i>								
<i>Gja3</i>								
	59	62	3	8	0	1	1	0

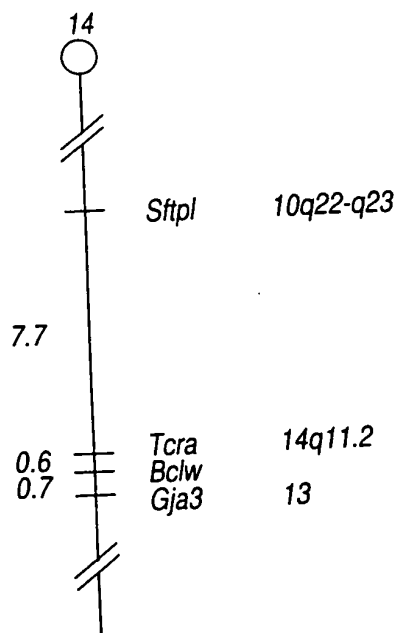


Fig. 6

- 11/26

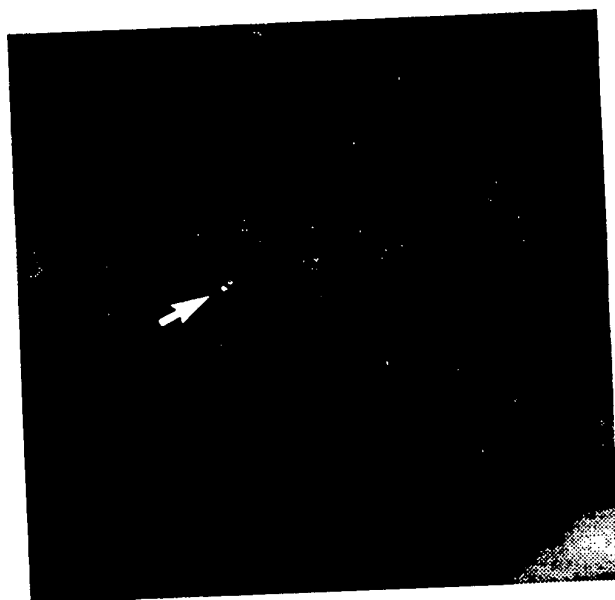


Fig. 7A



Fig. 7B

- 12/26

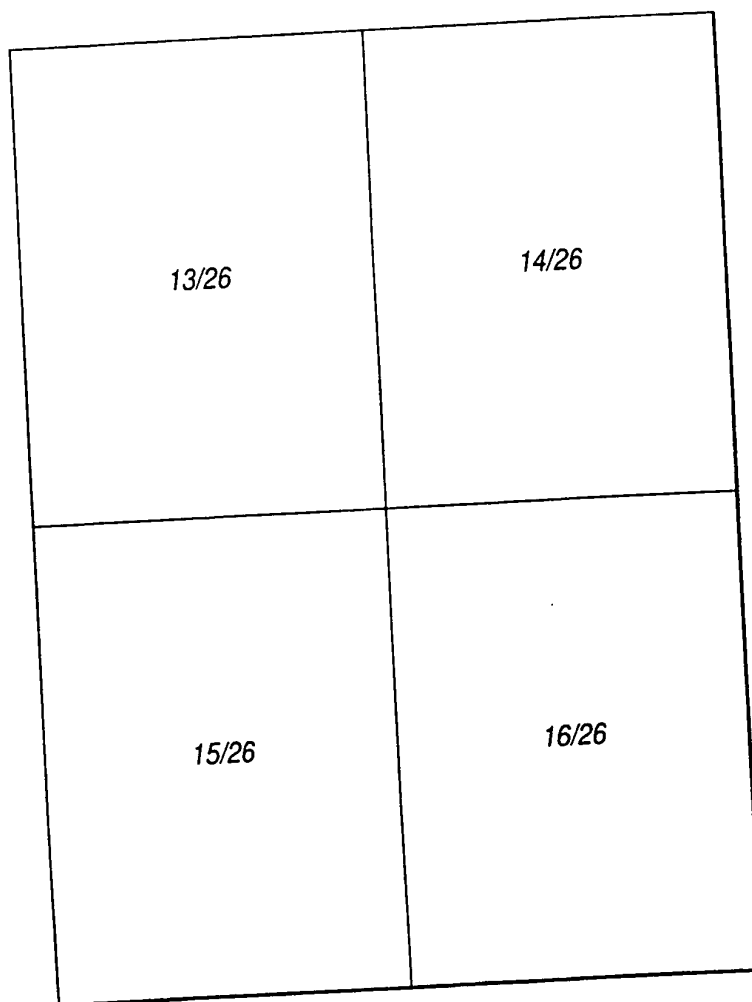


Fig. 8

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S1

Bc12	MAHAGRTGYD	NREI VMKYIH	YKLSORGYEW
Bc1x _LMSQS	NRELVVDFLS	YKLSQKGYSW
Bc1w	.MATPASAPD	TRALVADFGV	YKLRQKGYVC
Ced9		D IEGFVVDYFT	HRIRONGMEW

MASG

Bak

Bax

Bc12	ASRDPVARTS	PLQTPAAPGA	AAGPAL....
Bc1x _L	PSWH.LADSP	AVNGATGHSS	SLDARE....
Bc1w
Ced9			

Bak	FRSYVFYRHQ	QEQEAEGVAA	PADPEMVTLP
BaxALLQG	FIQDRAGRMG	GEAPELALDP
Bik			

S2

Bc12	MSROLHLTP	FTARGREATV	VEELERDG.V
Bc1x _L	LTSQLHITP	GTAYQSEEQV	VNELERDG.V
Bc1w	LAAQLHVTP	GSAQQRETQV	SDELEQGG.P
CED9	FCEQLLAVP	RISFSLYQDV	VRTVGNAQTD

Fig. 8 (i)

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DAGDVGAAPP GAAPAGIFS SQPGHTPHTA	60
SQFSDVEENR TEAPEGTESE METPSAINGN	54
GAGPGE	35
	99

QGP G PPR Q EC G EPAL P SASE EQVAQDTEEV	34
MDGS G EQPR G GGPTS S EQI MKTG	23

BH3

NH1

...SPVPPVV HLT L RQAGDDFSRRYRRDFAE	113
...VIPMAAV KQALREAGDEFELRYRRAFS	107
...GPAADPL HQAMRAAGDEEETRFRRTFSD	63
HEMMRVMTIFEKKHAENFET	132

* *

LQPSSTMGQV GRQ L AIIGDDINRRYDSEFOT	95
VPQDASTKKL SECLKRI G DELDS . . NMELOR	78
LACIGDEM D	

△

△

BH1

...NWGRIV AFFEFGG . . V	MCVESVNRE	165
...NWGRIV AFFSFGG . . A	LCVESVDKE	158
...NWGRIV AFFVEGA . . A	LCAESVNKE	114
QCPMSYGR L I GLISEGGFVA AKMMESV . . E		190

Fig. 8 (ii)

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Bak	MLQHLOPTA	ENAYEYETKI	ATSLFESG. I
Bax	MIAAVD..T	DSPREVEFRV	AADMESDGNF

S3

Bc12	MSPLVDNIAL	WMTEYLNHRH.	LHTWIQDNGG
Bc1x _L	MOVLVSRIAA	WMATYLNDRH.	LEPWIQENG
Bc1w	MEPLVGQVQE	WMVAYLETR.	LADWTHSSGG
Ced9	LOGQVRNLFV	YTSLFIKTRI	RNNWKEHNRS

Bak	LTGFLGQVTR	FVVDFMLHHC	IARWIAQRGG
Bax	VPELIRTIMG	WTLDFLRERL	LG.WIQDQGG

Bc12	DFSWLSLKT	LSLAL.VGAC	ITLGAYLGHK
Bc1x _L	RKGQERFNRW	FLTGMTVAGV	VLLGSLFSRK
Bc1w	EGNWASVRTV	LTGAVALGAL	VTVGAFASK

BakGP	ILNVLVVLGV	VLLGQFVVR
BaxTPT	WQTVTIFVAG	VTASLTIWK

Fig. 8 (iii)

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....NWGRVV ALLGEGY..	R	LALHVYQHG	146
....NWGRVV ALFYFAS..	K	LVLKALCTK	128
	Δ		
BH2			
WDAFVELYG.	PSMRPLF		210
WDTFVELYG.	NNAAAES		203
WAEFTALYGD	GALEEARRLR		163
WDDEMTL.G.			218
WVAALNLGN.			185
WDGLLSYFG.			166
			239
			233
			193
FFKS			211
KMG			192

Fig. 8 (iv)

SUBSTITUTE SHEET (RULE 26)

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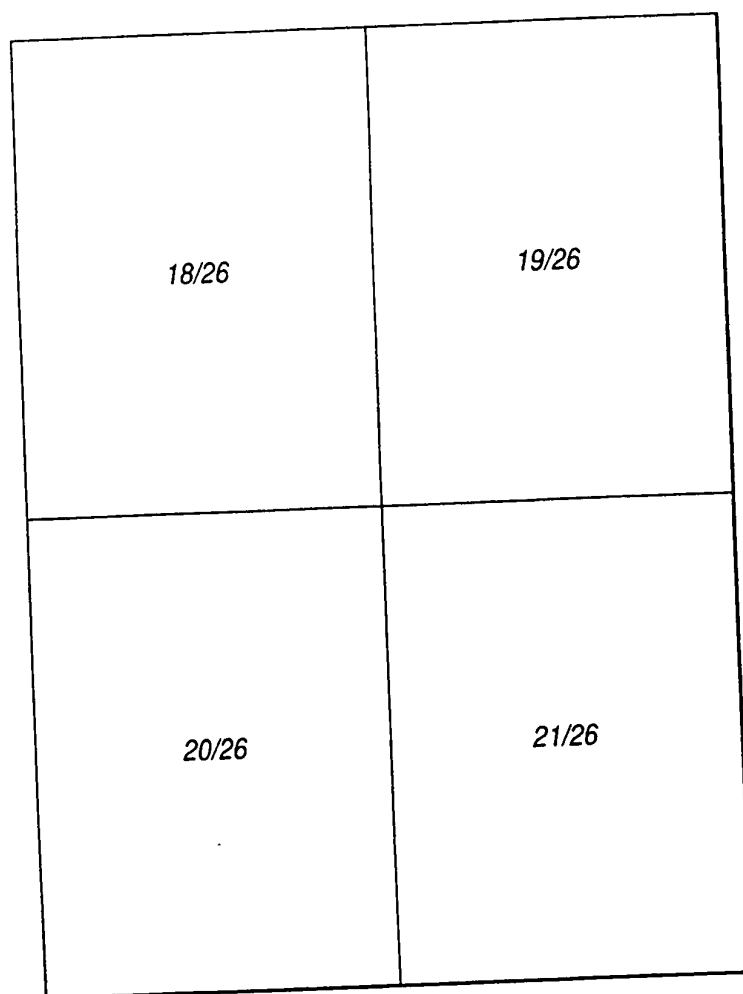


Fig. 9A

18/26

ATG GCG ACC CCA GCC TCG GCC CCA GAC
Met Ala Thr Pro Ala Ser Ala Pro Asp
1 5

TTT GTA GGT TAT AAG CTG AGG CAG AAG
Phe Val Gly Tyr Lys Leu Arg Gln Lys
20 25

CCC GGG GAG GGC CCA GCA GCT GAC CCG
Pro Gly Glu Gly Pro Ala Ala Asp Pro
35 40

GCT GGA GAT GAG TTC GAG ACC CGC TTC
Ala Gly Asp Glu Phe Glu Thr Arg Phe
50 55

GCG GCT CAG CTG CAT GTG ACC CCA GGC
Ala Ala Gln Leu His Val Thr Pro Gly
65 70

CAG GTC TCC GAC GAA CTT TTT CAA GGG
Gln Val Ser Asp Glu Leu Phe Gln Gly
85

GTA GCC TTC TTT CTC TTT GGG GCT GCA
Val Ala Phe Phe Leu Phe Gly Ala Ala
100 105

Fig. 9A (i)

SUBSTITUTE SHEET (RULE 26)

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ACA CGG GCT CTG GTG GCA GAC	48
Thr Arg Ala Leu Val Ala Asp	
10 15	
GGT TAT GTC TGT GGA GCT GGC	96
Gly Tyr Val Cys Gly Ala Gly	
30	
CTG CAC CAA GCC ATG CGG GCA	144
Leu His Gln Ala Met Arg Ala	
45	
CGG CGC ACC TTC TCT GAT CTG	192
Arg Arg Thr Phe Ser Asp Leu	
60	
TCA GCC CAG CAA CGC TTC ACC	240
Ser Ala Gln Gln Arg Phe Thr	
75 80	
GGC CCC AAC TGG GGC CGC CTT	288
Gly Pro Asn Trp Gly Arg Leu	
90 95	
CTG TGT GCT GAG AGT GTA AAC	336
Leu Cys Ala Glu Ser Val Asn	
110	

Fig. 9A (ii)
SUBSTITUTE SHEET (RULE 26)

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AAG GAG ATG GAA CCA CTG GTG GGA CAA
 Lys Glu Met Glu Pro Leu Val Gly Gln
 115 120

TAC CTG GAG ACG CGG CTG GTC GAC TGG
 Tyr Leu Glu Thr Arg Leu Val Asp Trp
 130 135

GCG GAG TTC ACA GCT CTA TAC GGG GAC
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp
 145 150

CGT CTG CGG GAG GGG AAC TGG GCA TCA
 Arg Leu Arg Glu Gly Asn Trp Ala Ser
 165

GCC GTG GCA CTG GGG GCC CTG GTA ACT
 Ala Val Ala Leu Gly Ala Leu Val Thr
 180 185

AAG TGA A
 Lys *

Fig. 9A (iii)

SUBSTITUTE SHEET (RULE 26)

- 21/26

GTG CAG GAG TGG ATG GTG GCC	384
Val Gln Glu Trp Met Val Ala	
125	
ATC CAC AGC AGT GGG GGC TGG	432
Ile His Ser Ser Gly Gly Trp	
140	
GGG GCC CTG GAG GAG GCG CGG	480
Gly Ala Leu Glu Glu Ala Arg	
155 160	
GTG AGG ACA GTG CTG ACG GGG	528
Val Arg Thr Val Leu Thr Gly	
170 175	
GTA GGG GCC TTT TTT GCT AGC	576
Val Gly Ala Phe Phe Ala Ser	
190	
	583

Fig. 9A (iv)

SUBSTITUTE SHEET (RULE 26)

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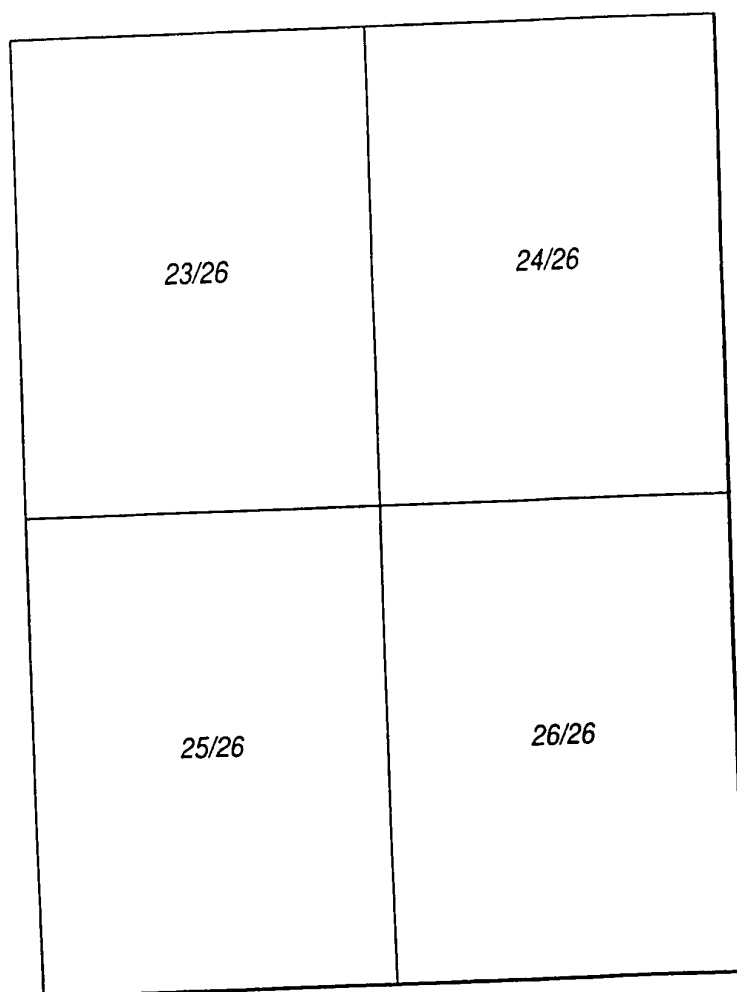


Fig. 9B

23/26

ATG CCG ACC CCA GCC TCA ACC CCA GAC
Met Pro Thr Pro Ala Ser Thr Pro Asp
1 5

TTT GTA GGC TAT AGG CTG AGG CAG AAG
Phe Val Gly Tyr Arg Leu Arg Gln Lys
20 25

CCT GGG GAA GGC CCA GCC GCC GAC CCG
Pro Gly Glu Gly Pro Ala Ala Asp Pro
35 40

GCT GGA GAC GAG TTT GAG ACC CGT TTC
Ala Gly Asp Glu Phe Glu Thr Arg Phe
50 55

GCC GCT CAG CTG CAC GTG ACC CCA GGC
Ala Ala Gln Leu His Val Thr Pro Gly
65 70

CAG GTT TCC GAC GAA CTT TTC CAA GGG
Gln Val Ser Asp Glu Leu Phe Gln Gly
85

GTG GCA TTC TTT GTC TTT GGG GCT GCC
Val Ala Phe Phe Val Phe Gly Ala Ala
100 105

Fig. 9B (i)

SUBSTITUTE SHEET (RULE 26)

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ACA CGC GCT CTA GTG GCT GAC	48
Thr Arg Ala Leu Val Ala Asp	
10 15	
GGT TAT GTC TGT GGA GCT GGG	96
Gly Tyr Val Cys Gly Ala Gly	
30	
CTG CAC CAA GCC ATG CGG GCT	144
Leu His Gln Ala Met Arg Ala	
45	
CGC CGC ACC TTC TCT GAC CTG	192
Arg Arg Thr Phe Ser Asp Leu	
60	
TCA GCC CAG CAA CGC TTC ACC	240
Ser Ala Gln Gln Arg Phe Thr	
75 80	
GGC CCT AAC TGG GGC CGT CTT	288
Gly Pro Asn Trp Gly Arg Leu	
90 95	
CTG TGT GCT GAG AGT GTC AAC	336
Leu Cys Ala Glu Ser Val Asn	
110	

Fig. 9B (ii)

SUBSTITUTE SHEET (RULE 26)

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AAA GAA ATG GAG CCT TTG GTG GGA CAA
 Lys Glu Met Glu Pro Leu Val Gly Gln
 115 120

TAC CTG GAG ACA CGT CTG GTC GAC TGG
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp
 130 135

GCG GAC TTC ACA GCT CTA TAC GGG GAC
 Ala Asp Phe Thr Ala Leu Tyr Gly Asp
 145 150

CGT CTG CGG GAG GGC AAC TGG GCA TGA
 Arg Leu Arg Glu Gly Asn Trp Ala *
 165

GCC GTG GCA CTG GGG GCC CTG GTA ACT
 Ala Val Ala Leu Gly Ala Leu Val Thr
 180 185

AAG TG
 Lys

Fig. 9B (iii)

SUBSTITUTE SHEET (RULE 26)

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GTC	CAG	GAT	TGG	ATC	GTG	GCC	384
Val	Gln	Asp	Trp	Ile	Val	Ala	
			125				
ATC	CAC	AGC	AGT	GGC	GGC	TGG	432
Ile	His	Ser	Ser	Gly	Gly	Trp	
			140				
GGG	GCC	CTG	GAG	GAC	GCA	CGG	480
Gly	Ala	Leu	Glu	Asp	Ala	Arg	
			155			160	
GTG	AGC	ACA	GTG	GTG	ACG	GGG	528
Val	Ser	Thr	Val	Val	Thr	Gly	
			170			175	
GTA	GGG	GCC	TTT	TTT	GCT	AGC	576
Val	Gly	Ala	Phe	Phe	Ala	Ser	
						190	
							582

Fig. 9B (iv)

SUBSTITUTE SHEET (RULE 26)

atg gcg acc cca gcc tcg gcc cca gac aca cgg gct ctg gtg gca gac 48
 Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
 1 5 10 15
 ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc 96
 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20 25 30
 ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca 144
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45
 gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg 192
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60
 gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80
 cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt 288
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95
 gta gcc ttc ttt gtc ttt ggg gct gca ctg tgt gct gag agt gtc aac 336
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110
 aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc 384
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
 115 120 125
 tac ctg gag acg cgg ctg gct gac tgg atc cac agc agt ggg ggc tgg 432
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140
 gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg 480
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
 145 150 155 160
 cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg 528
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
 165 170 175
 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190
 aag tgaa 583
 Lys

Figure 9A

	A	S1			
Bclw	MATPAST	DT KALVADFVGY KLRQKGY	VCG	AGPGEGPAAD	PLHQAMRAAG 5 0
Bclw-Rox	MATPAST	DT RALVADFVGY KLRQKGY	VCG	AGPGEGPAAD	PLHQAMRAAG 5 0

			S2		
Bclw	DEFETRFRRT	FSDLAAQLHV	TPGSAQQ	FT QVSDELFGGG	PNWGRLVAFF 1 0 0
Bclw-Rox	DEFETRFRRT	FSDLAAQLHV	TPGSAQQ	FT QVSDELFGGG	PNWGRLVAFF 1 0 0

			E		S3	
Bclw	VFGA	ALCAES	VNKEMEPLVG	QVQDWMVAYL	ETRLAD	WIHS SGGWAEFTAL 1 5 0
Bclw-Rox	VFGA	ALCAES	VNKEMEPLVG	QVQDWMVAYL	ETRLAD	WIHS SGGWAEFTAL 1 5 0

Bclw	YGD	GALEEAR	RLREGNWASV	RTVLTGAVAL	GALVTVGAF	ASK* 1 9 3
Bclw-Rox	ARVREMEEEA	EKLKELQNEV	EKQNMMSPPP	GNAGPVIMSL	EEKMEADARS	2 0 0

Bclw-Rox	IYVGNVDYGA	TAELEAHFH	GCGSVNRVTI	LCDKFSGHPK	GFAYIEFS	SDK 2 5 0

Bclw-Rox	ESVRTSLALD	ESLFRGRQIK	VIPKRTNRPG	ISTTDRGFPR	SRYRARTTNY	3 0 0

Bclw-Rox	NSSRSRFYSG	FNSRPRGRIY	RGRARATSWY	SPY*		3 3 3

Genetic Map

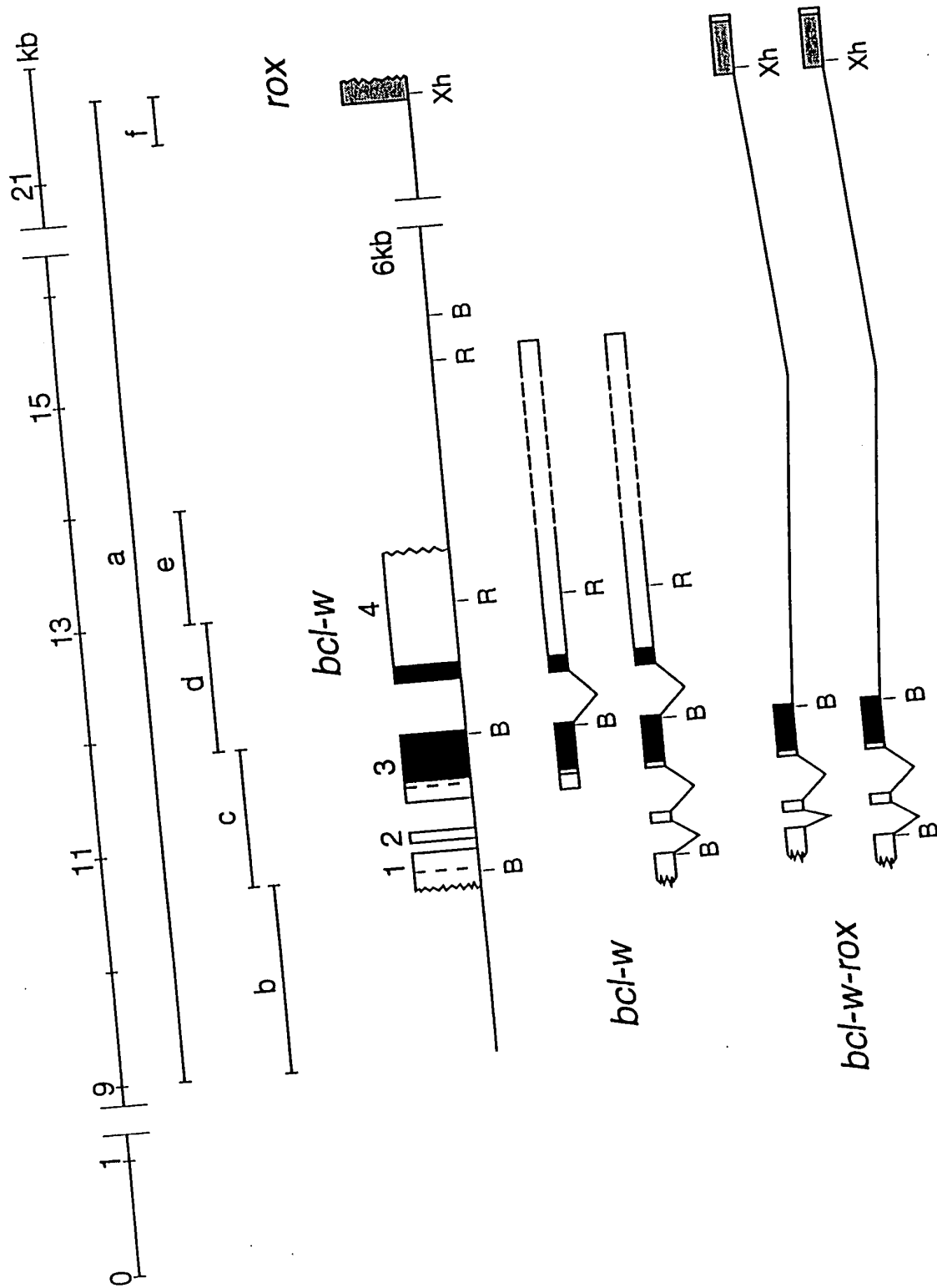


FIGURE 2

3.7 →

J774
P388D1
RAW 309Cr
RAW 264.7
3MES/RAF
LYH7
BAF3
W274
W265
W3BD-
FDC-P1
FD/Bcl-2
416B
W112.1
W105.7
EL4.1
YAC1
W404.1
ABLS8.1

m0
myeloid
B

FIGURE 3

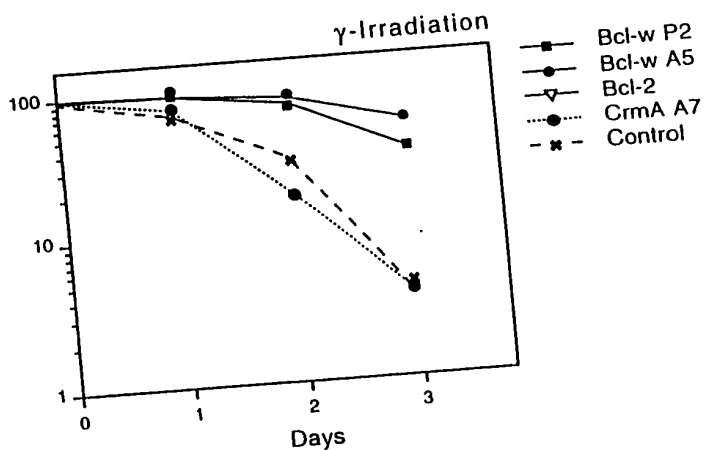
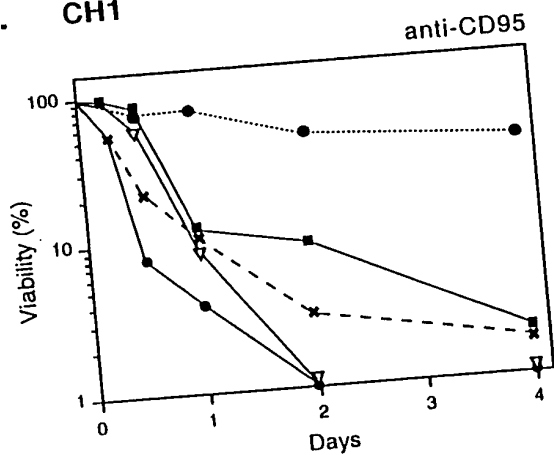
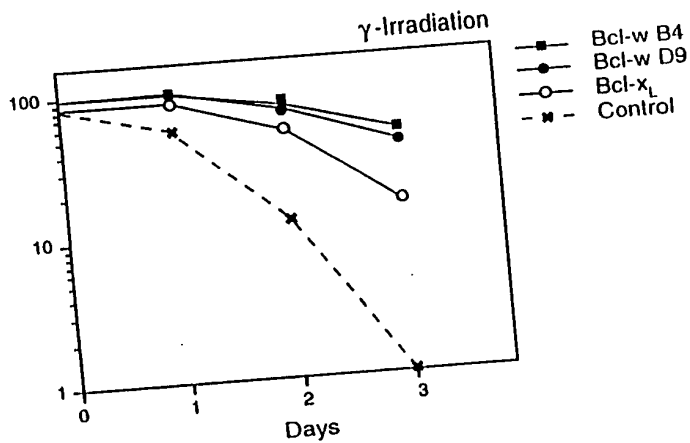
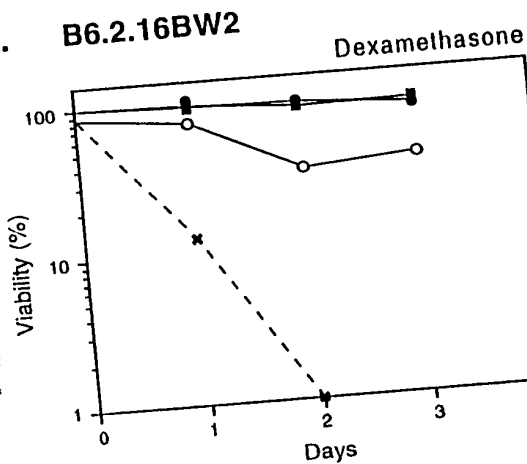
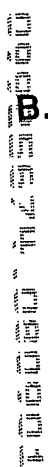
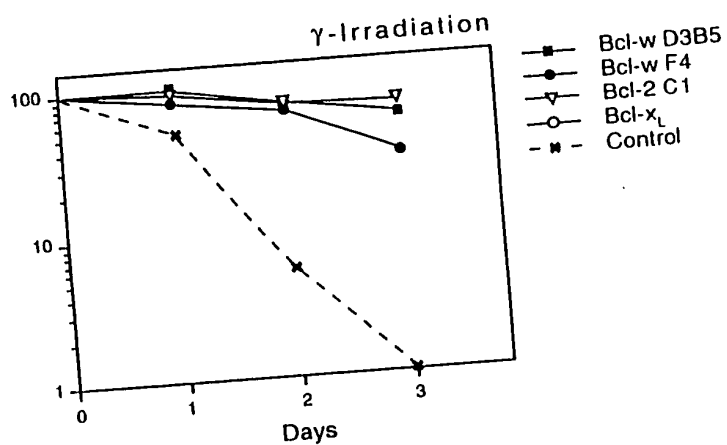
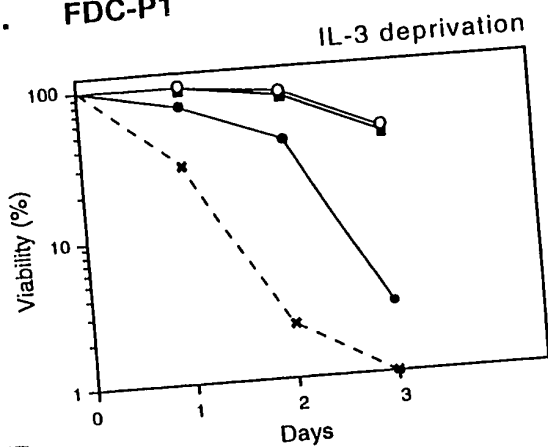


FIGURE 5

Gene	59	62	3	8	0	1	1	0
<i>Sftp1</i>	Black	White	White	Black	White	Black	White	Black
<i>Tcra</i>	Black	White	Black	White	White	Black	White	Black
<i>Bclw</i>	Black	White	Black	White	Black	White	White	Black
<i>Gja3</i>	Black	White	Black	White	Black	White	Black	White

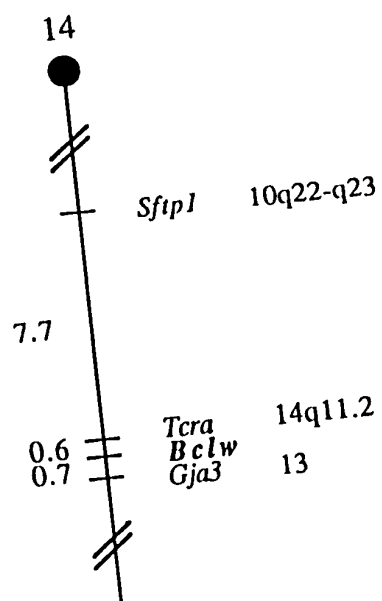


FIGURE 6

S1

Bcl2 MANAGRTGYD NREIUMKYIH VKLSRGTEW DAGDVGAAPP GAAPAPGIFS 50
 BclxLMSQS NRELVDVFLS VKLSKGYSW SQFSDVEENR TEAPEGTESE 44
 Bclw .MATPASAPD TIALVADFGV VKLROKGVVC GAGPGE..... 35

BakMASG QGPEPFR EC CEPALPASE 24
 BaxMDGSGEP PR GCGETSBEQI 19

Bcl2 SQPGHTPHTA ASRDPVARTS PLQTPAAPGA AAGPAL.....SPVPPVV 93
 BclxL METPSAINGN PSWH.LADSP AVNGATGHSS SLDARE.....VIPMAAV 86
 BclwGPAADPL 42

Ba EQVAQDTEEV FRSYVYRHQ QEQAEGVAA PADPEVTLF LQPSSTMGQV 74
 Bax MKTG.....ALLQG FIOLRAGRMG GEAPETALDE VPQDASTKKL 59

BH3 NH1 S2 BH1

Bcl2 HLTLPQAGDE PSREYRDEFA EMSRELHLIT FTARGRFATV VEELFRDG.V 142
 BclxL KQALFEAGDE PELFYRRAES CLTSQLHITP GTMYQSFEQV VNELFRDG.V 135
 Bclw HQAMEAAGDE FETHRETES ELAAQLHVTE GSAQQRFETQV SDELEQGS.P 91

Bak GRODAIAGDD INRRYDSEFO TMLQHLQPTA ENAYEYETKI TSLEESG.I 123
 Bax SECHKRIGDE LDS..NMELQ RMIAAVD..T DSPREVEFRV AADMESDGNF 105
 Bik IACRIGDE MD

S3 BH2

Bcl2 NNGRIVAFPE FCGVMCVESV NREMSPLVDN IALMITEYLN RH.LHTWIQD 191
 BclxL NNGCRIVAFPS FCGALCVESV DKEMQVLVSR IAAMMATYLN DH.LEFWIQE 184
 Bclw NNGGLVAFEV FGAALCAESV NKEMEPVUGQ VQEMNVAVIE TR.LADWIHS 140

Bak NNGRIVAFPE FGYRLATHVY QHGLTGFLGQ VTRFVVDTL HHCIARWIAQ 173
 Bax NNGRIVAFPE FASKVLEKAL CTKVP ELIRT IMGWTLDEER ERLLG.WIQD 154

Bcl2 NNGGDAFVEL YG.....PSMRPL FDFSWSLKT LLSLAL.VGA CITLMAYLGH 239
 BclxL NNGGDTFVEL YG.....NNAAAE SRKGQERFNR WFLTGMTVAG VVLLSLESR 233
 Bclw SEGGAZFTA YGDALEEARRL REGNWASVRT VLTGAVALGA LUTVGAFFAS 193

Bak RGGWVAALNL GN.....G PILNVLVVLG VVLLGQFVVR 211
 Bax QGGWDGLLSY FG.....TP TWQVTIFVA GULTASLTIV 192

FIGURE 8

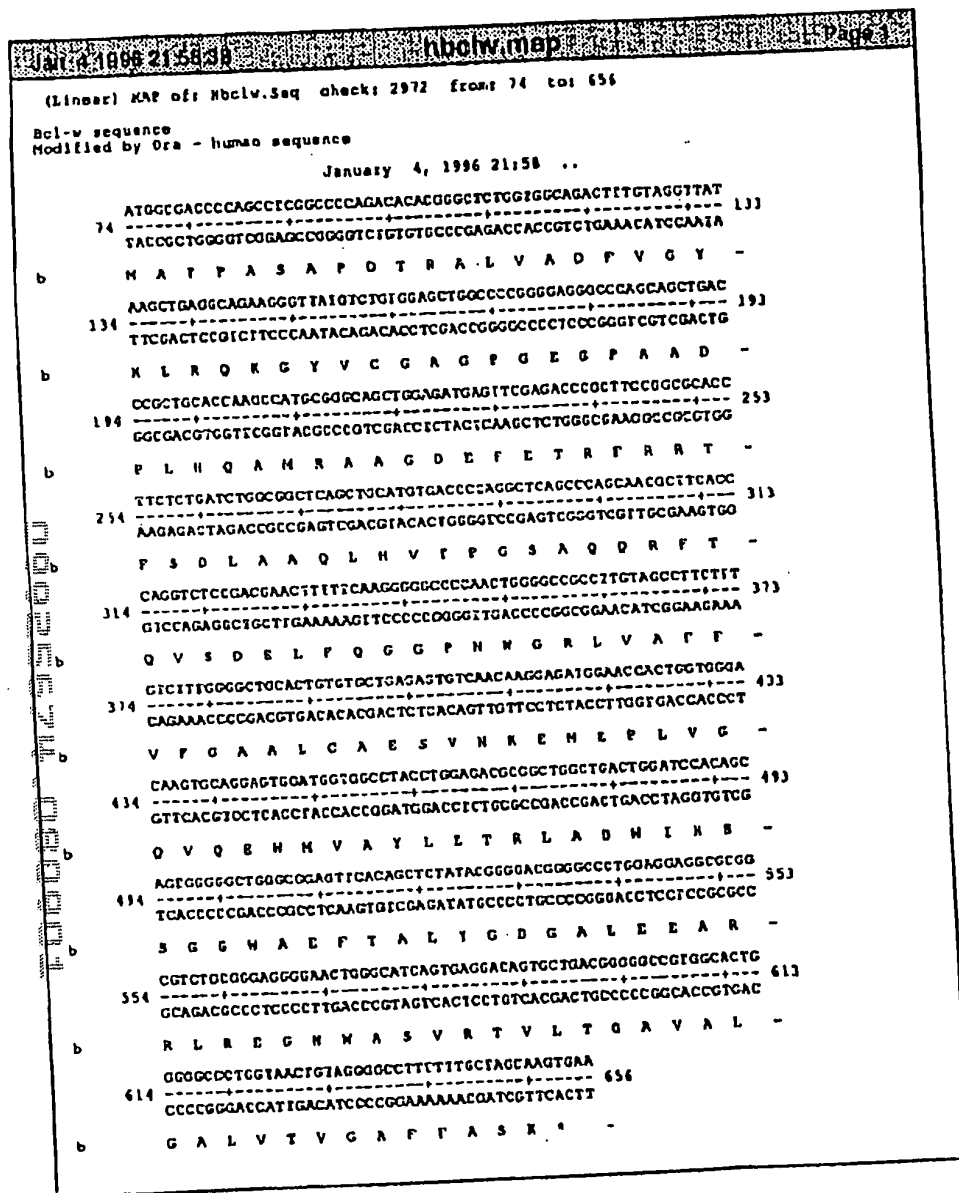


FIGURE 9A

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FIGURE 9B